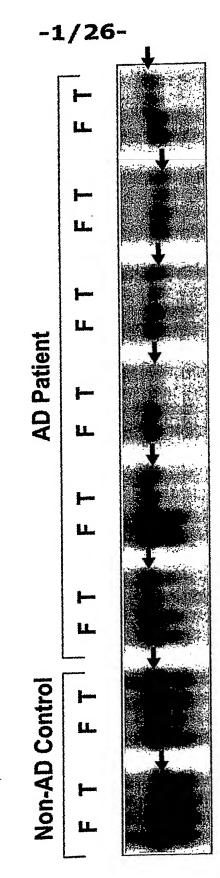
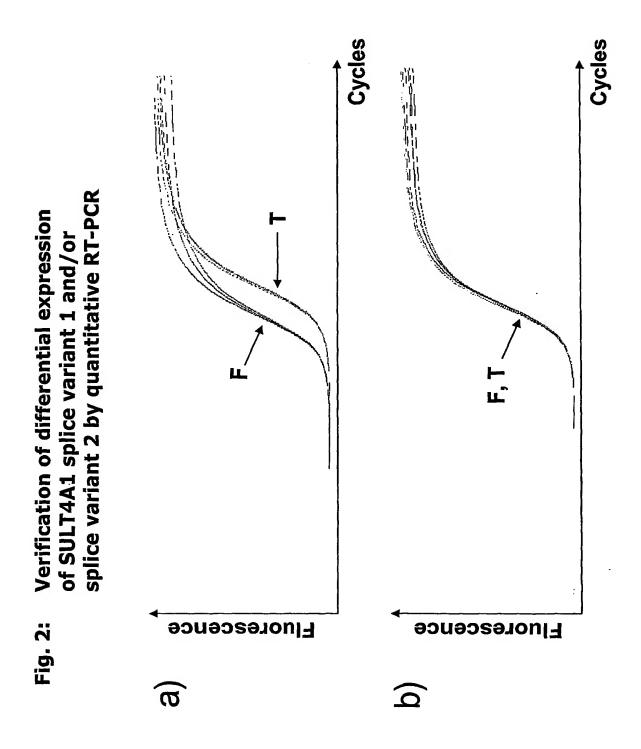
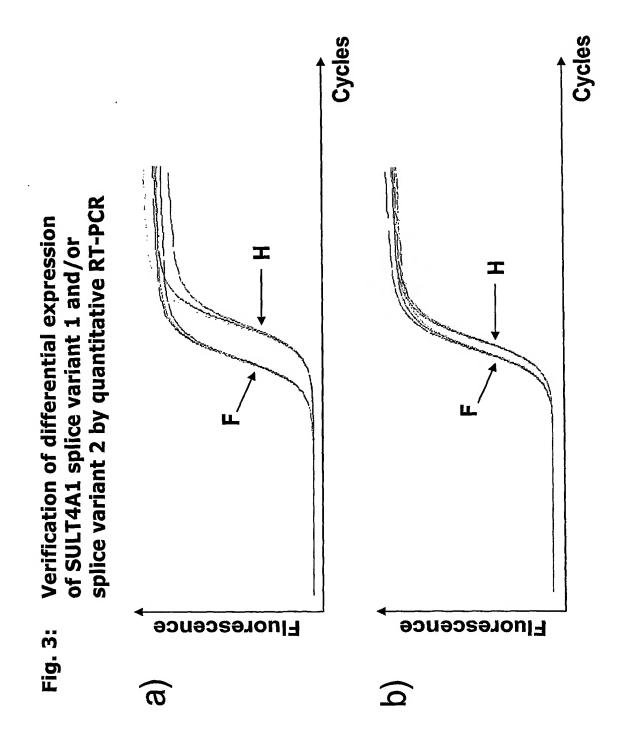
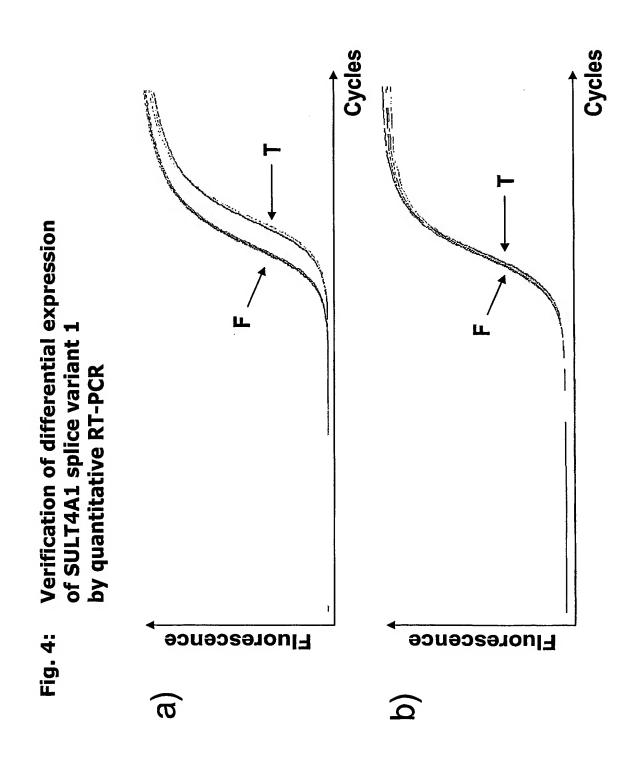
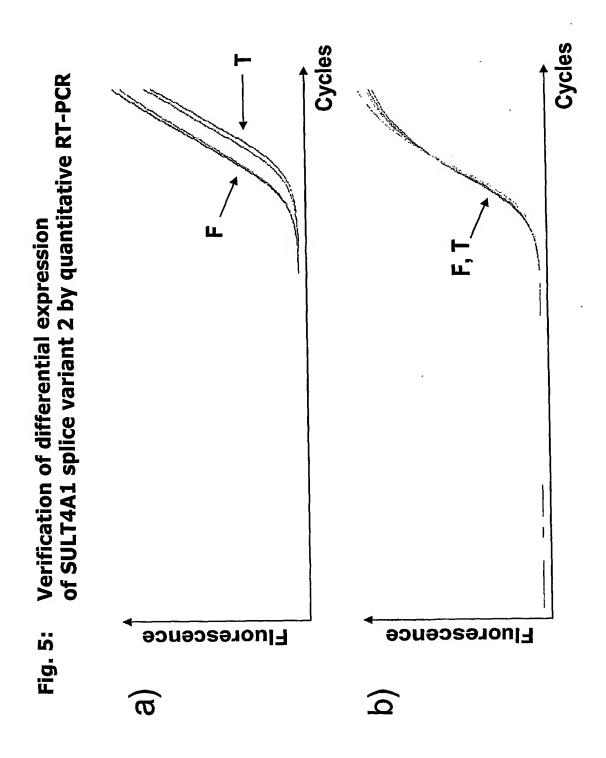
Fig. 1: Identification of differentially expressed genes in a fluorescence differential display screen











-,/7

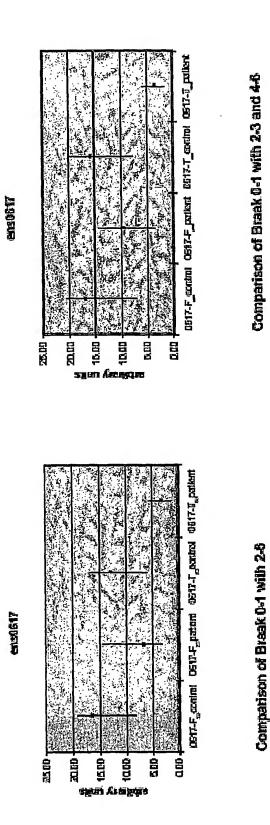
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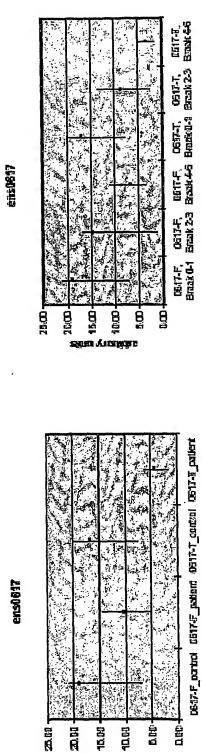
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expression of SULT4A1sv1 and/or SULT4A1sv2 Fig. 6: Analysis of absolute mRNA

Companison of Break 0-3 with 4-5

Comparison of Braek 0-2 with Break 3-6





T, Brank 4-5 051797-OSITEM. T gettest Comparison of Braak 0-1 with 2-3 and 4-6 Comparison of Braak 0-2 with Braak 3-6 06172시-1, Erzyk 도쿄 DEITEM. T partie 16, Brank D-1 Fig. 7: Analysis of absolute mRNA expression of SULT4A1sv1 ensole Tevr SERVICE TRAIN F. Brazile 4-5 Cellrant-DE13PA-F\_potent DESTENT. OSTTENT. F\_control ESTON-F, Brank P-1 30 8 몸 8 8 8 国 000 8 加る 10.四 ä र्स्टिका एक सिवाद sym Amyres del Text CB17sv1. T\_patiant Companison of Break 0-1 with 2-8 Companison of Break 0-3 with 4-6 Detrayt-**6817241**-T<sub>a</sub>contino ensolitizari chs08/734f OSITEAL F pedient OSITAN-F\_pattert Coltant. Deligny. Feentral 400 88 900 10.00 8 88 908 김명 1000 908 400 87 80 12.00 A STATE OF THE PERSON NAMED IN spin Congres

### -8/26-

# Fig. 8: SEQ ID NO. 1: amino acid sequence of human SULT4A1 protein, splice variant 1

#### Length: 284 aa

1 MAESEAETPS TPGEFESKYF EFHGVRLPPF CRGKMEEIAN FPVRPSDVWI
51 VTYPKSGTSL LQEVVYLVSQ GADPDEIGLM NIDEQLPVLE YPQPGLDIIK
101 ELTSPRLIKS HLPYRFLPSD LHNGDSKVIY MARNPKDLVV SYYQFHRSLR
151 TMSYRGTFQE FCRRFMNDKL GYGSWFEHVQ EFWEHRMDSN VLFLKYEDMH
201 RDLVTMVEQL ARFLGVSCDK AQLEALTEHC HQLVDQCCNA EALPVGRGRV

251 GLWKDIFTVS MNEKFDLVYK QKMGKCDLTF DFYL

### -9/26-

## Fig. 9: SEQ ID NO. 2: amino acid sequence of human SULT4A1 protein, splice variant 2

Length: 171 aa

1 MAESEAETPS TPGEFESKYF EFHGVRLPPF CRGKMEEIAN FPVRPSDVWI

51 VTYPKSVGYG SWFEHVQEFW EHRMDSNVLF LKYEDMHRDL VTMVEQLARF

101 LGVSCDKAQL EALTEHCHQL VDQCCNAEAL PVGRGRVGLW KDIFTVSMNE

151 KFDLVYKQKM GKCDLTFDFY L

### -10/26-

# Fig. 10: SEQ ID NO. 3: nucleotide sequence of human SULT4A1 cDNA, splice variant 1

Length: 2419 bp

1			ATGGCGGAGA		
51	ACCCCGGGGG		CAAGTACTTC		
101	GCCGCCCTTC		AGATGGAGGA		TTCCCGGTGC
151	GGCCCAGCGA			CCAAGTCCGG	
201	CTGCAGGAGG			GGCGCTGACC	CCGATGAGAT
251	CGGCTTGATG	AACATCGACG	AGCAGCTCCC	GGTCCTGGAG	TACCCACAGC
301		CATCATCAAG		CTCCCCGCCT	CATCAAGAGC
351	CACCTGCCCT	ACCGCTTTCT	GCCCTCTGAC	CTCCACAATG	GAGACTCCAA
401	GGTCATCTAT	ATGGCTCGCA	ACCCCAAGGA	TCTGGTGGTG	TCTTATTATC
451	AGTTCCACCG	CTCTCTGCGG	ACCATGAGCT	ACCGAGGCAC	CTTTCAAGAA
501	TTCTGCCGGA	GGTTTATGAA	TGATAAGCTG	GGCTACGGCT	CCTGGTTTGA
551	GCACGTGCAG	GAGTTCTGGG	AGCACCGCAT	GGACTCGAAC	GTGCTTTTTC
601	TCAAGTATGA	AGACATGCAT	CGGGACCTGG	TGACGATGGT	GGAGCAGCTG
651	GCCAGATTCC	TGGGGGTGTC	CTGTGACAAG	GCCCAGCTGG	AAGCCCTGAC
701	GGAGCACTGC	CACCAGCTGG	TGGACCAGTG	CTGCAACGCT	GAGGCCCTGC
751	CCGTGGGCCG	GGGAAGAGTT	GGGCTGTGGA	AGGACATCTT	CACCGTCTCC
801	ATGAATGAGA	AGTTTGACTT	GGTGTATAAA	CAGAAGATGG	GAAAGTGTGA
851	CCTCACGTTT	GACTTTTATT	TATAATAACA	GAAACAACAA	CCTGCATGCT
901	CACAATACCC	AGACAGTCTA	CTAGCCAAAA	GTCCTGTATG	CATTCATTTA
951	TTCCTTGCTG	GACAAACTCT	GGAAGCAGCG	TGTGAAACAG	CGGGGGAAGG
1001	GAAGAGCGGC	GTGAGCGGAG	GGAGTGTGAT	GATTCCCAAC	CGAAGCAGCT
1051	GTCTCGCCTT	TAGAACGTGC	AGCCTCTCCA	TGTCTGATTA	CAAACAGTCT
1101	CCACATTGCA	GTTCCAATGG	CCTGGACCGT	AAGGATAAAG	CCTGTAATAT
1151	ATGCAACTAG	AATGTCTGCC	TTTTCAACCC	CGTATTATTG	TATTTTATAG
1201	AGCTTTTCAC	TGGAAATCTA	CATAAATGTC	AGTAAACCAA	ATAAAAGTTC
1251	ATTTCCAAGG	GGAATCAGGA	GCGAGCCACA	CCCGAATGGT	AGAAAGATCT
1301	CAGGGTTAAC	TCTTTATTTT	TGTAGTTTTA	TTATCTAAGG	CACAGCCATT
1351	CTGTTCTCAC	TTGGTTCTGA	GATAGTGGTG	AGAACAGAGG	ATGAGTTGGG
1401	TCTGTTGGGG	GGAATCTGGA	CACTTGTTTA	TTCTGACGGA	GTTCACTTCT
1451	TCAGAACCTT	CCTGAAATGA	GCAGAAATTG	TTCACTAGGT	CTTCAGAATG
1501	GACGTCCTTC	TGCCAGAGAC	TTCCAGCGGG	CGGCTCCAAA	GGCCCAATGC
1551	AGAGGAGCCC	GCGGAGCATG	TGCTGAGGGA	AGTCTGCCTG	GTGAGGCTGG
1601	CAGGTGGGAG	TCTAATGCAG	TCAGGAGCAT	TTGCATGCAG	TGGGTGGAGA
1651	GTCGGCCACC	AAAGGACCGA	GTTGCGCTCG	GAATTTGAGC	TGAATTCCAC
1701	AGCCTTACTT	TGTTTCCTGA	AGTGATAGCC	TACTAATGCT	GGCAAGCAGA
1751	TGCTTAATAG	TAAATTTCTA	AAATCCCCGG	GTCTTTATCA	TTCAGTTTGT
1801	TCTGTGCACC	TGAGGCGCTC	AGCCGTGGGA	GGACCATTTI	GCGAGTGTAG
1851	CCCTGTTTCA	CTCGGATCAG	GTTGGCACGG	CCGCCTGCGT	GTCTGTCCAC
1901	CTCATCCCTC	CGTGTATCTG	AGGGAGTAAA	GGTGAGGTCI	TTATTGCTTC
1951	ACTGCCTAAT	TTTCTCACCC	ACATTCGCTG	AAGCGATGGA	GAGTCGGGGG
2001	CCAGTAGCCA	GCCAACCCCG	TGGGGACCGG	GGTTGTCTGT	CATTTATGTG
2051	GCTGGAAAGC		GTGGTCAGGA		

### -11/26-

2101	GTCTCCGTTC	TTGGTGCTGT	ATTTGAAACG	GGTGTAGAGA	GAAGCTTGTG
2151	TTTTTGTTTG	TAATGGGGAG	AAGCGTGGCC	AGGCAGGTGG	CACGTGGCAT
2201	CGCATGGTGG	GCTCGGCAGC	ACCTTGCCTG	TGTTTCTGTG	AGGGAGGCTG
2251	CTTTCTGTGA	AATTTCATTT	ATATTTTTCT	ATTTTTAGTA	CTGTATGGAT
2301	GTTACTGAGC	ACTACACATG	ATCCTTCTGT	GCTTGCTTGC	ATCTTTAATA
2351	AAGACATGTT	CCCGGCGTTG	CAAAAAAAAA	AAAAAAAAA	AAAAAAAAA
2401	AAAAAAAAA	AAAAAAAA			

### -12/26-

Fig. 11: SEQ ID NO. 4: nucleotide sequence of human SULT4A1 cDNA, splice variant 2

Length: 2080 bp

1	CCC ACCCCCA	cadacadaa	3mccccc3c3	CCCACCCCCA	an according
51.		AGTTCGAGAG		GCGAGGCCGA GAGTTCCATG	
101	GCCGCCCTTC		AGATGGAGGA		
					TTCCCGGTGC
151	GGCCCAGCGA		GTCACCTACC	CCAAGTCCGT	GGGCTACGGC
201	TCCTGGTTTG	AGCACGTGCA	GGAGTTCTGG	GAGCACCGCA	TGGACTCGAA
251	CGTGCTTTTT	CTCAAGTATG	AAGACATGCA	TCGGGACCTG	GTGACGATGG
301	TGGAGCAGCT	GGCCAGATTC	CTGGGGGTGT	CCTGTGACAA	
351	GAAGCCCTGA		CCACCAGCTG	GTGGACCAGT	GCTGCAACGC
401		CCCGTGGGCC	GGGGAAGAGT	TGGGCTGTGG	
451		CATGAATGAG	AAGTTTGACT	TGGTGTATAA	
501	GGAAAGTGTG		TGACTTTTAT	TTATAATAAC	
551	ACCTGCATGC	TCACAATACC	CAGACAGTCT	ACTAGCCAAA	
601	GCATTCATTT	ATTCCTTGCT	GGACAAACTC	TGGAAGCAGC	
651	GCGGGGGAAG		CGTGAGCGGA	GGGAGTGTGA	TGATTCCCAA
701	CCGAAGCAGC	TGTCTCGCCT	TTAGAACGTG	CAGCCTCTCC	ATGTCTGATT
751	ACAAACAGTC	TCCACATTGC	AGTTCCAATG	GCCTGGACCG	TAAGGATAAA
801	GCCTGTAATA	TATGCAACTA	GAATGTCTGC	CTTTTCAACC	CCGTATTATT
851	GTATTTTATA	GAGCTTTTCA	CTGGAAATCT	ACATAAATGT	CAGTAAACCA
901	AATAAAAGTT	CATTTCCAAG	GGGAATCAGG	AGCGAGCCAC	ACCCGAATGG
951	TAGAAAGATC	TCAGGGTTAA	CTCTTTATTT	TTGTAGTTTT	ATTATCTAAG
1001	GCACAGCCAT	TCTGTTCTCA	CTTGGTTCTG	AGATAGTGGT	GAGAACAGAG
1051	GATGAGTTGG	GTCTGTTGGG	GGGAATCTGG	ACACTTGTTT	ATTCTGACGG
1101	AGTTCACTTC	TTCAGAACCT	TCCTGAAATG	AGCAGAAATT	GTTCACTAGG
1151	TCTTCAGAAT	GGACGTCCTT	CTGCCAGAGA	CTTCCAGCGG	GCGGCTCCAA
1201	AGGCCCAATG	CAGAGGAGCC	CGCGGAGCAT	GTGCTGAGGG	AAGTCTGCCT
1251	GGTGAGGCTG	GCAGGTGGGA	GTCTAATGCA	GTCAGGAGCA	TTTGCATGCA
1301	GTGGGTGGAG	AGTCGGCCAC	CAAAGGACCG	AGTTGCGCTC	GGAATTTGAG
1351	CTGAATTCCA	CAGCCTTACT	TTGTTTCCTG	AAGTGATAGC	CTACTAATGC
1401	TGGCAAGCAG	ATGCTTAATA	GTAAATTTCT	AAAATCCCCG	GGTCTTTATC
1451	ATTCAGTTTG	TTCTGTGCAC	CTGAGGCGCT	CAGCCGTGGG	AGGACCATTT
1501	TGCGAGTGTA	GCCCTGTTTC	ACTCGGATCA	GGTTGGCACG	GCCGCCTGCG
1551	TGTCTGTCCA	CCTCATCCCT	CCGTGTATCT	GAGGGAGTAA	AGGTGAGGTC
1601	TTTATTGCTT	CACTGCCTAA	TTTTCTCACC	CACATTCGCT	GAAGCGATGG
1651	AGAGTCGGGG	GCCAGTAGCC	AGCCAACCCC	GTGGGGACCG	GGGTTGTCTG
1701	TCATTTATGT	GGCTGGAAAG	CACCCAAAGT	GGTGGTCAGG	AGGGTCGCTG
1751	CTGTGGAAGG	GGTCTCCGTT	CTTGGTGCTG	TATTTGAAAC	GGGTGTAGAG
1801	AGAAGCTTGT	GTTTTTGTTT	GTAATGGGGA	GAAGCGTGGC	CAGGCAGGTG
1851	GCACGTGGCA	TCGCATGGTG	GGCTCGGCAG	CACCTTGCCT	GTGTTTCTGT
1901	GAGGGAGGCT	GCTTTCTGTG	AAATTTCATT	TATATTTTTC	TATTTTTAGT
1951	ACTGTATGGA	TGTTACTGAG	CACTACACAT	GATCCTTCTG	TGCTTGCTTG
2001	CATCTTTAAT	AAAGACATGT	TCCCGGCGTT	GCAAAAAAAA	AAAAAAAAA
2051	AAAAAAAAA	ААААААААА	ААААААААА		

-13/26-

Fig. 12: SEQ ID NO. 5

Length: 32 bp

1 GATTGCATCT TTAATAAAGA CATGTTCCCG GC

### -14/26-

### Fig. 13: SEQ ID NO. 6: nucleotide sequence of human SULT4A1 coding sequence

#### Length: 855 bp

1	ATGGCGGAGA	GCGAGGCCGA	GACCCCCAGC	ACCCCGGGGG	AGTTCGAGAG
51	CAAGTACTTC	GAGTTCCATG	GCGTGCGGCT	GCCGCCCTTC	TGCCGCGGGA
101	AGATGGAGGA	GATCGCCAAC	TTCCCGGTGC	GGCCCAGCGA	CGTGTGGATC
151	GTCACCTACC	CCAAGTCCGG	CACCAGCTTG	CTGCAGGAGG	TGGTCTACTT
201	GGTGAGCCAG	GGCGCTGACC	CCGATGAGAT	CGGCTTGATG	AACATCGACG
251	AGCAGCTCCC	GGTCCTGGAG	TACCCACAGC	CGGGCCTGGA	CATCATCAAG
301	GAACTGACCT	CTCCCCGCCT	CATCAAGAGC	CACCTGCCCT	ACCGCTTTCT
351	GCCCTCTGAC	CTCCACAATG	GAGACTCCAA	GGTCATCTAT	ATGGCTCGCA
401	ACCCCAAGGA	TCTGGTGGTG	TCTTATTATC	AGTTCCACCG	CTCTCTGCGG
451	ACCATGAGCT	ACCGAGGCAC	CTTTCAAGAA	TTCTGCCGGA	GGTTTATGAA
501	TGATAAGCTG	GGCTACGGCT	CCTGGTTTGA	GCACGTGCAG	GAGTTCTGGG
551	AGCACCGCAT	GGACTCGAAC	GTGCTTTTTC	TCAAGTATGA	AGACATGCAT
601	CGGGACCTGG	TGACGATGGT	GGAGCAGCTG	GCCAGATTCC	TGGGGGTGTC
651	CTGTGACAAG	GCCCAGCTGG	AAGCCCTGAC	GGAGCACTGC	CACCAGCTGG
701	TGGACCAGTG	CTGCAACGCT	GAGGCCCTGC	CCGTGGGCCG	GGGAAGAGTT
751	GGGCTGTGGA	AGGACATCTT	CACCGTCTCC	ATGAATGAGA	AGTTTGACTT
801	GGTGTATAAA	CAGAAGATGG	GAAAGTGTGA	CCTCACGTTT	GACTTTTATT
851	TATAA	•			

### -15/26-

### Fig. 14: Alignment of SEQ ID NO. 5 with human SULT4A1sv1 and SULT4A1sv2 cDNAs

Length: 32 bp

SEQ ID NO.5 : SULT4A1sv1

SEQ ID NO.5 : SULT4A1sv2

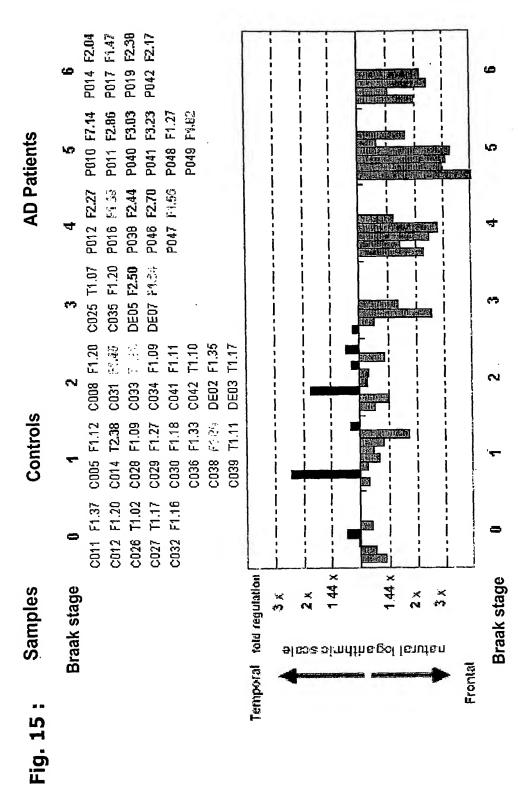
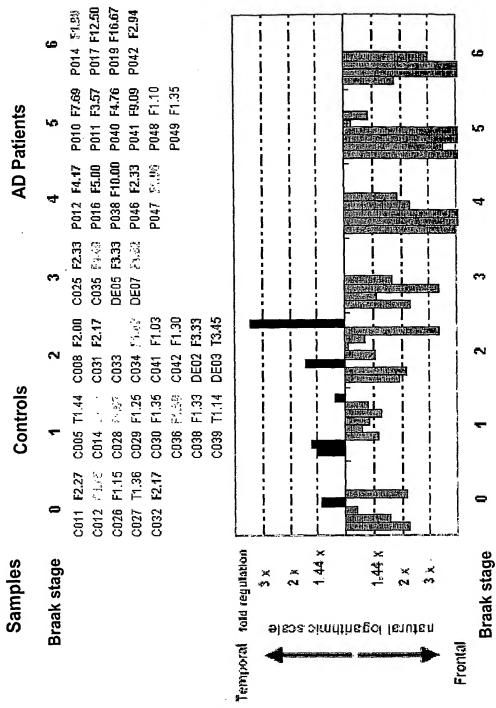


Fig. 16 :



sample ∆ (fold) (hippocampus/ frontal cortex)

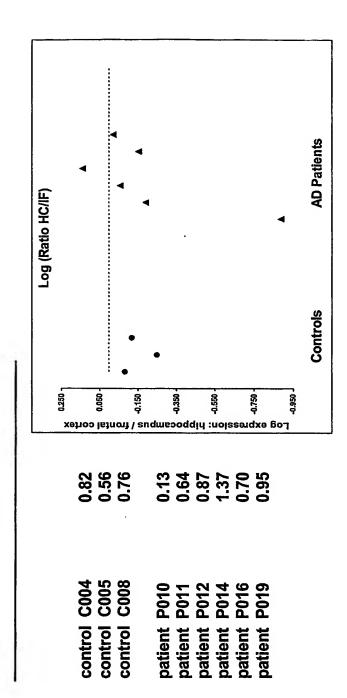


Fig. 17

SULT4A1 protein in neuroglioma cells Fig. 18: Immunofluorescence analysis of

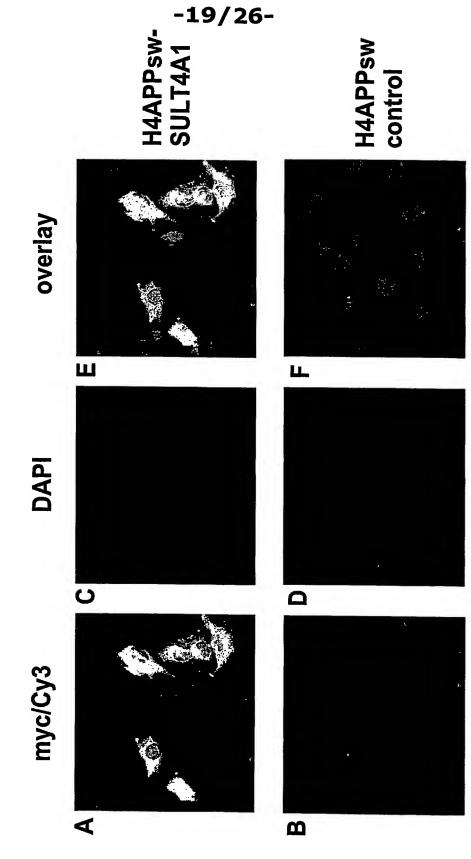


Fig. 19: Effect of trophic factor deprivation on SULT4A1 over-expressing cells

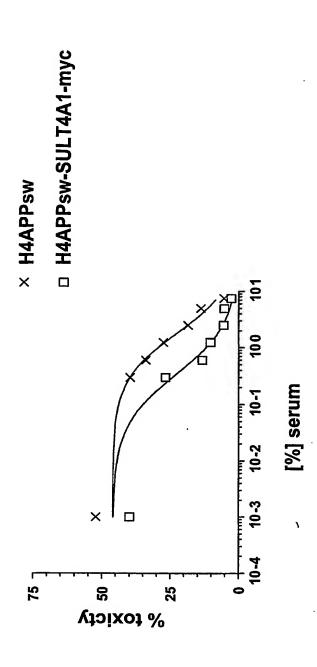


Fig. 20: Generation of Sult4A1 deficient mice

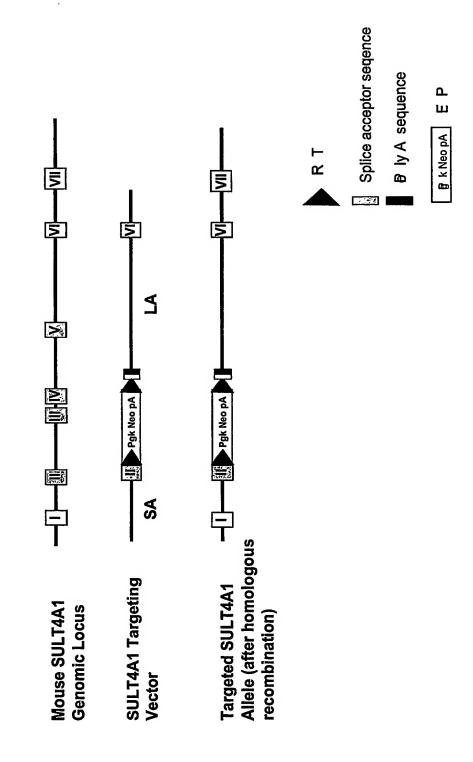
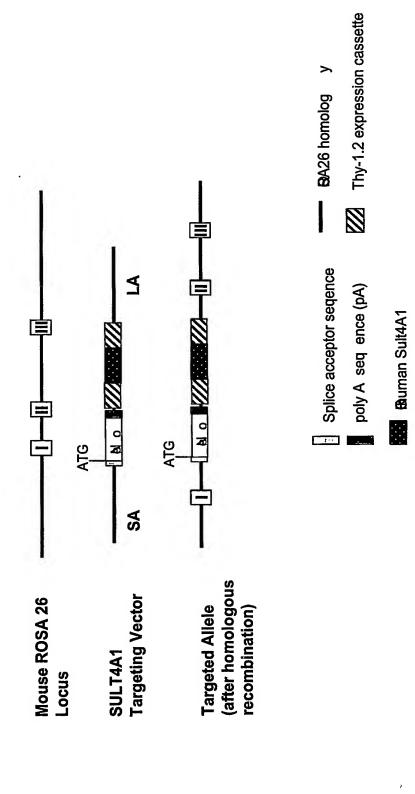


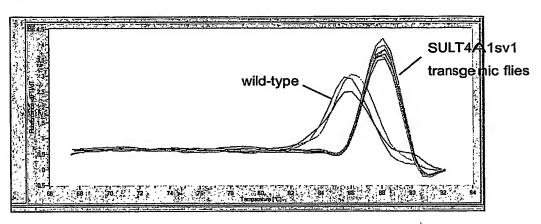
Fig. 21: Generation of Sult4A1 trangenic mice



### -23/26-

Fig. 22: Transgenic expression of Sult4A1

### A



В

name	cycle number	mean	stdev	error [%]	efficiency (expression normalized to housekeeping gene)	
SULT4A1#3	21.34	21.300	0.14422205	0.67709883	1.8 times more than	
SULT4A1#3	21.14				SULT4A1#8; 2.7 times	
SULT4A1#3	21.42				more than SULT4A1#22	
			•			
SULT4A1#8	23.79	23.917	0.11676187	0.48820292		
SULT4A1#8	23.94					
SULT4A1#8	24.02				<del></del>	
SULT4A1#22		23.915	0.03535534	0.1478375		
SULT4A1#22	23.94					
SULT4A1#22	23.89					

E= 10<sup>(-1/slope)</sup> slope= -2.960 E= 2.176

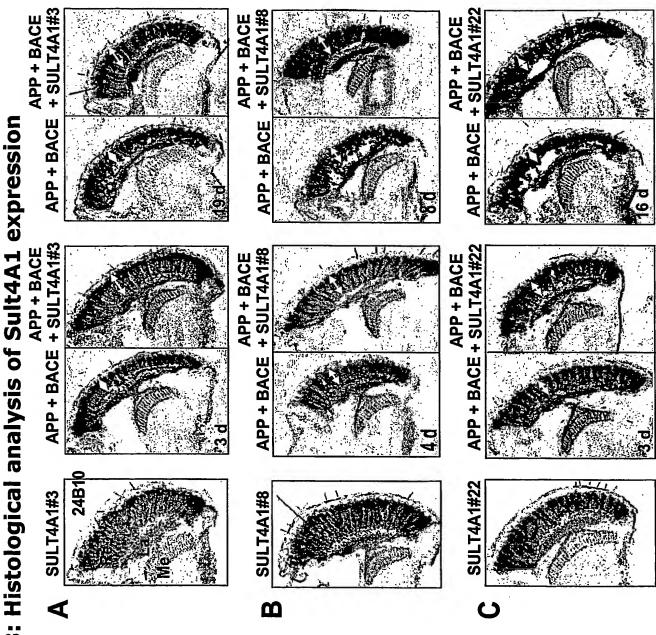
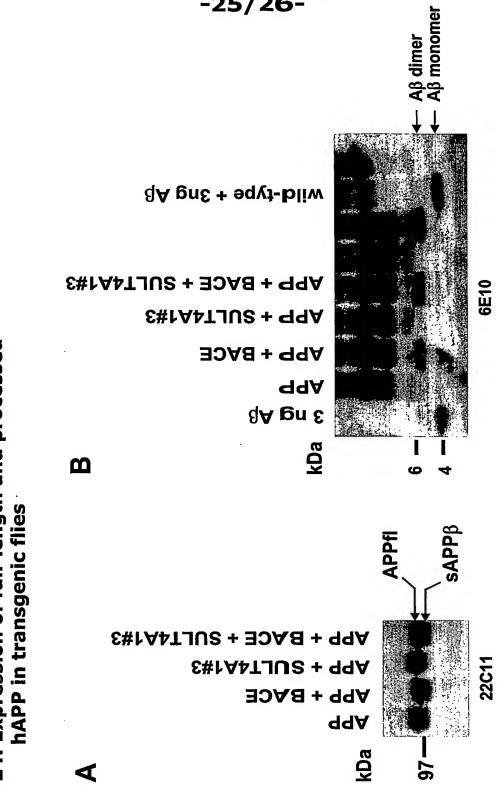


Fig. 23: Histological analysis of Sult4A1 expression

Fig. 24: Expression of full-length and processed hAPP in transgenic flies



-25/26-

Fig. 25: Thioflavin S positive amyloid plaques in transgenic flies

APP + BACE + PsnL235P + SULT4A1#3 38d Ω APP + BACE + PsnL235P 38d 4

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